TCGACCCACGCGTCCGGGAGGATCGGGAGTCGCGGGAGGATGGGCCGCCGCTAGGCTCGCACTCCGGA
CGCGCCTCGC
AGTGCGCAGGGTGGGTGCCCCGCGCCTGCAGCGTCCGCCGGGGCGGCGCGGCGGGAGGTGGCCGACAG
GCTCCGGGCC
TCGCAGCCTCAGCCCCCGGCCCAGCGCGCTTTCCGACGGCGGCGCCGCGCCGAGCCACCCGCC
CGCCCAAGGTCTCTCGCGGGCGGGAGAACGGAAAACTCCCAACTTCCTGAGTTCTAAAGTTCCTGTTG
CTTCAGACAA
TGGATGAGCAATCACAAGGAATGCAAGGGCCACCTGTTCCTCAGTTCCAACCACAGAAGGCCTTACGA
CCGGATATGG
GCTATAATACATTAGCCAACTTTCGAATAGAAAAGAAAATTGGTCGCGGACAATTTAGTGAAG
TTTATAGAGCAGCCTGTCTCTTGGATGGAGTACCAGTAGCTTTAAAAAAAGTGCAGATATTTGATTTA
ATGGATGCCA
AAGCACGTGCTGATTGCATCAAAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAA
TATTATGCAT
CATTCATTGAAGATAATGAACTAAACATAGTTTTGGAACTAGCAGATGCTGGCGACCTATCCA
GAATGATCAAGCATTTTAAGAAGCAAAAGAGGCTAATTCCTGAAAGAACTGTTTGGAAGTATTTTGTT
CAGCTTTGCA
GTGCATTGGAACACATGCATTCTCGAAGAGTCATGCATAGAGATATAAAACCAGCTAATGTGTTCATT
ACAGCCACTG
GGGTGGTAAAACTTGGAGATCTTGGGCTTGGCCGGTTTTTTCAGCTCAAAAACCACAGCTGCAC
ATTCTTTAGTTGGTACGCCTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACTTCAAA
TCTGACATCT
GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACAAAATGAAT
TTATACTCAC
TGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCCTTCAGATCACTATTCAGAAGAAC
TCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAGAGAAGCGACCAGACGTCACCTATGTTTAT
GACGTAGCAA
AGAGGATGCATGCATGCACTGCAAGCAGCTAAACATGCAAGATCATGAAGAGTGTAACCAAAGTAATT
GAAAGTATTT
TGTGCAAAGTCGTACCTSCCCATTTATGTCTGGGTGTTAAGATTAATATTTCAGAGCTAGTGT
GCTCTGAATCCTTAACCAGTTTTCATATAAGCTTCATTTTGTACCAGTCACCTAAATCACCTCCTTGC
AACCCCCAAA
TGACTTTGGAATAACTGAATTGCATGTTAGGAGAGAAAATGAAACATGATGGTTTTGAATGGCTAAAG
GTTTATAGAA
TTTCTTACAGTTTTCTGCTGATAAATTGTGTTTAGATAGACTGTCAGTGCCAAATATTGAAGG
TGCAGCTTGGCACACATCAGAATAGACTCATACCTGAGAAAAAGTATCTGAACATGTGACTTGTTTCT
TTTTTAGTAA
TTTATGGACATTGAGATGAACACAATTGTGAACTTTTGTGAAGATTTTATTTTTAAACGTTTGAAGTA
CTAGTTTTAG
TTCTTAGCAGAGTAGTTTTCAAATATGATTCTTATGATAAATGTAGACACAAACTATTTGAGA
AACATTTAGAACTCTTAGCTTATACATTCAAAATGTAACTATTAAATGTGAAGATTTGGGGACAAAAT
GTGAGTCAGA
CACTGAAGAGTTTTTTGTTTTGTTTTAATATTTTTGATATTCTCTTTGCATTGAAATGGTATAAATGA
ATCCATTTAA
AAAGTGGTTAAGGATTTGTTTAGCTGGTGTGATAATAATTTTTAAAGTTGCACATTGCCCAAG
GCTTTTTTTGTGTGTTTTTATTGTTGTTTGTACATTTGAAAAATATTCTTTGAATAACCT'TGCAGTAC
TATATTTCAA

Fig. 1

TTTCTTTATAAATTTAAGTGCATTTTAACTCATAATTGTACACTATAATATAAGCCTAAGTTTTTATT
CATAAGTTTT
ATTGAAGTTCTGATCGGTCCCCTTCAGAAATTTTTTTTATATTATTCTTCAAGTTACTTTCTTA
TTTATATTGTATGTGCATTTTATCCATTAATGTTTCATACTTTCTGAGAGTATAATACCCTTTTAAAA
GATATTTGGT
ATACCAATACTTTTCCTGGATTGAAAACTTTTTTTTAAACTTTTTAAAATTTGGGCCACTCTGTATGCA
TATGTTTGGT
CTTGTTAAAGAGGAAGAAAGGATGTGTGTTATACTGTACCTGTGAATGTTGATACAGTTACAA
TTTATTTGACAAGGTTGTAATTCTAGAATATGCTTAATAAAATGAAAACTGGCCATGACTACAGCCAG
AACTGTTATG
AGATTAACATTTCTATTGAGAAGCTTTTGAGTAAAGTACTGTATTTGTTCATGAAGATGACTGAGATG
GTAACACTTC
GTGTAGCTTAAGGAAATGGGCAGAATTTCGTAAATGCTGTTGTGCAGATGTGTTTTCCCTGAA
TGCTTTCGTATTAGTGGCGACCAGTTTCTCACAGAATTGTGAAGCCTGAAGGCCAAGAGGAAGTCACT
GTTAAAGGAC
TCTGTGCCATCTTACAACCTTGGATGAATTATCCTGCCAACGTGAAAACCTCATGTTCAAAGAACACT
TCCCTTTAGC
CGATGTAACTGCTGGTTTTGTTTTTCATATGTGTTTTTCTTACACTCATTTGAATGCTTTCAA
GCATTTGTAAACTTAAAAAAAAANWAWAAAGGGCAAAAAGTCTGAACCCTTGTTTTCTGAAATCTAATC
AGTTATGTAT
GGTTTCTGAAGGGTAATTTTATTTTGGAATAGGTAAAGCGAAACCTGTTTTGTCWTGTTTTTCCTGAG
GGCTAGATGC
ATTTTTTTTCTCACACTCTTAATGACTTTTAACATTTATACTGAGCATCCATAGATATATTCC
TAGAAGTATGAGAAGAATTATTCTTATTGACCATTAATGTCATGTTCATTTTAATGTAATATAATTGA
GATGAAATGT
TCTCTGGTTGGAACAGATACTCTCTTTTTTTTTTCTTGCAATCTTTAAGAATACATAGATCTAAAATTC
ATTAGCTTGA
CCCCTCAAAGTAACTTTTAAGTAAAGATTAAAGCTTTTCTTCTCAGTGAATATATCTGCTAGA
AGGAAATAGCTGGGAAGAATTTAATGATCAGGGAAATTCATTATTTCTATATGTGGAAACTTTTTGCT
TCGAATATTG
TATCTTTTTAAATCTAAATGTTCATATTTTTCCTGAAGAAACCACTGTGTAAAAATCAAATTTTAATT
TTGAATGGAA
TAATTTCAAAGAACTATGAAGATGATTTGAAGCTCTAATTTATATAGTCACCTATAAAATGTT
CTTTATATGTGTTCATAAGTAAATTTTATATTGATTAAGTTAAACTTTTGAATTGATTTGAGGAGCAG
TAAAATGAAA
GCTATATCTATTNCTAAACCYTATTTAGACATTGGKACCAGTTACCCAGGTGAAAATAKGGAGTAACT
TTGTTTTGTA
TGGTAAGGTTTAGGAATGGNGGATGAAGGGTATCTCTATATAAATAAAGTGCTCAACAATGTG
CAATGATTGTAAATTTAGTAAGATATTACAGCCATTTCATGAATGCTTTACCATTCAACATAGTATCT
ATTACAAAAC
ACCTTTCTTGTATCCATATACTTCAGGTGTTGCTGTTAACATTTACTATGATATTTATTTTAACCAAA
ATGTTACTCA
CATTAAATGTTTATTCTTTAAAATGAATGTATTATGTTTTTAACCCACAAATGCATACTTACC
CTGTGCCTCATATTTCAATAGTACTGTAATATGGACATCTTTTGTGAAATACTTTTATTTTGTTATGC
TTTAAATATA
CATACAAAAAGATTTCTGTTATTAGCTTTGAAAATTGTATAATATCCTAATATAAACAAAAATATAAA
AATAAAAATG
AATACAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGG

Fig. 1 (continued)

MDEQSQGMQGPPVPQFQPQKALRPDMGYNTLANFRIEKKIGRGQFSEVYRAACLLDGVPVALKKVQIF
DLMDAKARAD
CIKEIDLLKQLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYFVQLC
SALEHMHSRR
VMHRDIKPANVFITATGVVKLGDLGLGRFFSSKTTAAHSLVGTPYYMSPERIHENGYNFKSDI
WSLGCLLYEMAALQSPFYGDKMNLYSLCKKIEQCDYPPLPSDHYSEELRQLVNMCINPDPEKRPDVTY
VYDVAKRMHA
CTASS

Fig. 1 (continued)

GTCGACCCACGCGTCCGGTGGAAGTATAATACTTTGTCATTATGAGATGTCGTCTCTCGG
TGCCTCCTTTGTGCAAATTAAATTTGATGACTTGCAGTTTTTTGAAAACTGCGGTGGAGG
AAGTTTTGGGAGTGTTTATCGAGCCAAATGGATATCACAGGACAAGGAGGTGGCTGTAAA
GAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCCTCAGTCACAGAAACAT
CATCCAGTTTTATGGAGTAATTCTTGAACCTCCCAACTATGGCATTGTCACAGAATATGC
TTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAGTGAGGAGATGGATATGGA
TCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTATTTACATATGGAGGC
TCCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGTTGTTATAGCTGCTGATGG
AGTACTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAACCATACAACACACATGTC
CTTGGTTGGAACTTTCCCATGGATGGCTCCAGAAGTTATCCAGAGTCTCCCTGTGTCAGA
AACTTGTGACACATATTCCTATGGTGTGGTTCTCTGGGAGATGCTAACAAGGGAGGTCCC
CTTTAAAGGTTTGGAAGGATTACAAGTAGCTTGGCTTGTAGTGGAAAAAAACGAGAGATT
AACCATTCCAAGCAGTTGCCCCAGAAGTTTTGCTGAACTGTTACATCAGTGTTGGGAAGC
TGATGCCAAGAAACGGCCATCATTCAAGCAAATCATTTCAATCCTGGAGTCCATGTCAAA
TGACACGAGCCTTCCTGACAAGTGTAACTCATTCCTACACAACAAGGCGGAGTGGAGGTG
CGAAATTGAGGCAACTCTTGAGAGGCTAAAGAAACTAGAGCGTGATCTCAGCTTTAAGGA
GCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAAAAGCTGACAGAGCA
GTCCAACACCCCGCTTCTCTTGCCTCTTGCTGCAAGAATGTCTGAGGAGTCTTACTTTGA
ATCTAAAACAGAGGAGTCAAACAGTGCAGAGATGTCATGTCAGATCACAGCAACAAGTAA
CGGGGAGGGCCATGGCATGAACCCAAGTCTGCAGGCCATGATGCTGATGGGCTTTGGGGA
TATCTTCTCAATGAACAAAGCAGGAGCTGTGATGCATTCTGGGATGCAGATAAACATGCA
AGCCAAGCAGAATTCTTCCAAAACCACATCTAAGAGAAGGGGGGAAGAAAGTCAACATGGC
TCTGGGGTTCAGTGATTTTGACTTGTCAGAAGGTGACGATGATGATGATGATGACGGTGA
GGAGGAGGATAATGACATGGATAATAGTGAATGAAAGCAGAAAGCAAAGTAATAAAATCA
CAAATGTTTGGAAAACACAAAAGTAACTTGTTTATCTCAGTCTGTACAAAAACAGTAAGG
AGGCAGAAAGCCAAGCACTGCATTTTTAGGCCAATCACATTTACATGACCGTAATTTCTT
ATCAATTCTACTTTTTATTTTTGCTTACAGAAAAACGGGGGGAGAATTAAGCCAAAGAAGT
ATATTTATGAATCAGCAAATGTGGTGCCTGATTATAGAAATTTGTGATCCTATATACAAT
ATAGGACTTTTAAAGTTGTGACATTCTGGCTTTTTCTTTTAATGAATACTTTTTAGTTTG
TATTTGACTTTATTTCCTTTATTCAAATCATTTTTAAAAACTTACATTTTGAACAAACAC
TCTTAACTCCTAATTGTTCTTTGACACGTAGTAATTCTGTGACATACTTTTTTTTTTCTTA
TAGCAATACACTGTAATATCAGAAATGGTTGGCCTGAGCAACCTAGTAAGACCTCGTCTC
TACTAATAATTAAAAAACTAGCTGGCATGGTAGCACACACCTGTAGTCCCAGATACTTGG
GAGGCCAAGGCAGGAGGATTGCTTGAGACCTAGCAATCAGTCAGGGCTGCAGTGAGCCAT
GATGGCACCACTGCACTCTAGCCTGGGCAAGAGAACAAGATCCTGTCTCAAAAAACAAAA
AAAAAAAAAAGGGCGGCCG

MSSLGASFVQIKFDDLQFFENCGGGSFGSVYRAKWISQDKEVAVK
KLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDMD
HIMTWATDVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTTHMS
LVGTFPWMAPEVIQSLPVSETCDTYSYGVVLWEMLTREVPFKGLEGLQVAWLVVEKNERL
TIPSSCPRSFAELLHQCWEADAKKRPSFKQIISILESMSNDTSLPDKCNSFLHNKAEWRC
EIEATLERLKKLERDLSFKEQELKERERRLKMWEQKLTEQSNTPLLLPLAARMSEESYFE
SKTEESNSAEMSCQITATSNGEGHGMNPSLQAMMLMGFGDIFSMNKAGAVMHSGMQINMQ
AKQNSSKTTSKRRGKKVNMALGFSDFDLSEGDDDDDDDGEEEDNDMDNSE

Fig. 2

CGGTGGTGGCGGCAGCGGCGGCTGCGGGGGCACCGGGCCGCGGCGCCACCATGGCCGTGC
GACAGGCGCTGGGCCGCGGCCTGCAGCTGGGTCGAGCGCTGCTGCTGCGCTTCACGGGCA
AGCCCGGCCGGGCCTACGGCTTGGGGCGGCCGGGCCCGGCGGCGGGCTGTGTCCGCGGGG
AGCGTCCAGGCTGGGCCGCAGGACCGGGCGCGGAGCCTCGCAGGGTCGGGCTCGGGCTTC
CTAACCGTCTCCGCTTCTTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGTTGCAGCGGC
AGTTCGTGGTGCGGGCCTGGGGCTGCGCGGGCCCTTGCGGCCGGGCAGTCTTTCTGGCCT
TCGGGCTAGGGCTGGGCCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGG
CCTGTCAGGAGATCCAGGCAATTTTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGG
ACACGAGACGCTTGCAGGGCTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTA
AGGGCTGCAGTGCTGCTGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGG
TGACAAAGAGCACCGGGTTGCTTCCAGGGAGAGGCCCAGGTACCAGTGCACCAGGAGAAG
GGCAGGAGCGAGCTCCGGGGGCCCCTGCCTTCCCCTTGGCCATCAAGATGATGTGGAACA
TCTCGGCAGGTTCCTCCAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAG
CGAGCCGAGTGGCCTTGGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAG
GTCCCAAGCAACTAGCCCCTCACCCCAACATCATCCGGGTTCTCCGCGCCTTCACCTCTT
CCGTGCCGCTGCTGCCAGGGGCCCTGGTCGACTACCCTGATGTGCTGCCCTCACGCCTCC
ACCCTGAAGGCCTGGGCCATGGCCGGACGCTGTTCCTCGTTATGAAGAACTATCCCTGTA
CCCTGCGCCAGTACCTTTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGC
TGCAGCTGCTGGAAGGCGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGA
AATCCGACAACATCCTTGTGGAGCTGGACCCAGACGGCTGCCCCTGGCTGGTGATCGCAG
ATTTTGGCTGCTGCCTGGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGT
ACGTGGATCGGGGCGGAAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCCTG
GCCCCAGGGCAGTGATTGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCT
ATGAAATCTTCGGGCTTGTCAATCCCTTCTACGGCCAGGGCAAGGCCCACCTTGAAAGCC
GCAGCTACCAAGAGGCTCAGCTACCTGCACTGCCCGAGTCAGTGCCTCCAGACGTGAGAC
AGTTGGTGAGGGCACTGCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCG
CAAATGTGCTTCATCTAAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGT
TAGACAAGATGGTTGGCTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGC
TCACAGAGAAGTGTTGTGTGGAAACAAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGT
GTGAAACGCTCTGCCAGGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTC
CCTGCATGGAGCTGGTGAATTACTAAAAGAACTTGGCATCCTCTGTGTCGTGATGGTCTG
TGAATGGTGAGGGTGGGAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAA
AAGGCCTCGGGCTTGGCAAATGGAAGAACTTGAGTGAGAGTTCAGTCTGCAGTCCTCTGC
TCACAGACATCTGAAAAGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGA
GGGGTAGGCCTGCATCCACAGAGAGGATCCAGGCCAAGGCACTGGCTGTCAGTGGCAGAG
TTTGGCTGTGACCTTTGCCCCTAACACGAGGAACTCGTTTGAAGGGGGCAGCGTAGCATG
TCTGATTTGCCACCTGGATGAAGGCAGACATCAACATGGGTCAGCACGTTCAGTTACGGG
AGTGGGAAATTACATGAGGCCTGGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGC
TACTGAATTATTAATCTCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTAAGTGTG
GGGATTTAAACTTGAGGGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATAT
TAAATGCAAATTTACAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCC

Fig. 3

```
                                                    Met Ala
Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala Leu Leu
         5               10               15

Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly Arg Pro
         20               25               30

Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp Ala Ala
35               40               45               50

Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro Asn Arg
                   55               60               65

Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg Leu Gln
              70               75               80

Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys Gly Arg
              85               90               95

Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu Glu Lys
    100              105              110

Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile Gln Ala
115              120              125              130

Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp Thr Arg
              135              140              145

Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln Ser Ile
              150              155              160

Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro Thr Leu
         165              170              175

Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro Gly Arg
180              185              190

Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala Pro Gly
195              200              205              210

Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile Ser Ala
              215              220              225
```

Fig. 3 (continued)

```
Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu Leu Val
        230             235             240

Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val Thr Tyr
        245             250             255

Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro Asn Ile
    260             265             270

Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu Pro Gly
275             280             285             290

Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His Pro Glu
            295             300             305

Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn Tyr Pro
        310             315             320

Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro Arg Leu
        325             330             335

Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His Leu Val
    340             345             350

Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile Leu Val
355             360             365             370

Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp Phe Gly
            375             380             385

Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe Ser Ser
        390             395             400

Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro Glu Val
        405             410             415

Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser Lys Ala
    420             425             430
```

Fig. 3 (continued)

```
Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly Leu Val
435             440             445             450

Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg Ser Tyr
                455             460             465

Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro Asp Val
                470             475             480

Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys Arg Pro
            485             490             495

Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp Gly Glu
        500             505             510

His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp
515             520             525             530

Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu
                535             540             545

Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu
            550             555             560

Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg
            565             570             575

Ala Ala Leu
```

Fig. 3 (continued)

GTCGACCCACGCGGTCCGCCCACGCGTTCCGGAGACATGTCTCTGTGTTTC
TCTCCCCTCCGCTTTTGAGTCCGTTGAAGACACAATTTCTCTCTGTCGGGT
GCTTAGGAGGAGCTCCATGAACATGTATTGAATTGGACTTAGCTGAACAG
GCTGCTGGTTGGCTGCCCAGAGGGGGCAGGCTGTGTTGCTGGGAGCCTTC
CAGCTCCCTGCAGCAGTCATGGGGCAGGGTTCCCCGAGTCCGTAATCCCC
ATTTCCACCTACTTTCCCTTAGTTATTTGATTCCCTGTCTGTCGTACTCAGC
TTAAGTGGAGCATCCCCTTTCCTGGGAGACACGAAGCAGGAAACACTGGC
AAATATCACAGCAGTGAGTTACGACTTTGATGAGGAATTCTTCAGCCAGA
CGAGCGAGCTGGCCAAGGACTTTATTCGGAAGCTTCTGGTTAAAGAGACC
CGGAAACGGCTCACAATCCAAGAGGCTCTCAGACACCCCTGGATCACGCC
GGTGGACAACCAGCAAGCCATGGTGCGCAGGGAGTCTGTGGTCAATCTGG
AGAACTTCAGGAAGCAGTATGTCCGCAGGCGGTGGAAGCTTTCCTTCAGC
ATCGTGTCCCTGTGCAACCACCTCACCCGCTCGCTGATGAAGAAGGTGCA
CCTGAGGCCGGATGAGGACCTGAGGAACTGTGAGAGTGACACTGAGGAG
GACATCGCCAGGAGGAAAGCCCTCCACCCACGGAGGAGGAGCAGCACCT
CCTAACTGGCCTGACCTGCAGTGGCCGCCAGGGAGGTCTGGGCCCAGCGG
GGCTCCCTTCTGTGCAGACTTTTGGACCCAGCTCAGCACCAGCACCCGGGC
GTCCTGAGCACTTTGCAAGAGAGATGGGCCCAAGGAATTCAGAAGAGCTT
GCAGGCAAGCCAGGAGACCCTGGGAGCTGTGGCTGTCTTCTGTGGAGGAG
GCTCCAGCATTCCCAAAGCTCTTAATTCTCCATAAAATGGGCTTTCCTCTG
TCTGCCATCCTCAGAGTCTGGGGTGGGAGTGTGGACTTAGGAAAACAATA
TAAAGGACATCCTCATCATCACGGGGTGAAGGTCAGACTAAGGCAGCCTT
CTTCACAGGCTGAGGGGGGTTCAGAACCAGCCTGGCCAAAAATTACACCAG
AGAGACAGAGTCCTCCCCATTGGGAACAGGGTGATTGAGGAAAGTGAACC
TTGGGTGTGAGGGACCAATCCTGTGACCTCCCAGAACCATGGAAGCCAGG
ACGTCAGGCTGACCAACACCTCAGACCTTCTGAAGCAGCCCATTGCTGGC
CCGCCATGTTGTAATTTTGCTCATTTTTATTAAACTTCTGGTTTACCTGATG
CTTGGCTTCTTTTAGGGCTACCCCCATCTCATTTCCTTTAGCCCGTGTGCCT
GTAACTCTGAGGGGGGGGCACCCAGTGGGGTGCTGAGTGGGCAGAATCTCA
GAAGGTCCTCCTGAACCGTCCGCGCAGGCCTGCAGTGGGCCTGCCTCCTC
CTTGCTTCCCTAACAGGAAGGTGTCCAGTTCAAGAGAACCCACCCAGAGA
CTGGGAGTGGTGGCTCACGCCTATAATCCCTGCGCTTTGGCAGTCCGAGG
CAGGGGAATTGCTTGAACTCAGGAGTTGGAGACCAGCCTGGGCAACATGG
CAAAACGCAGTCTGTACAAAAAATACAAAAAATTAGCCAGGTGTAGGGGT
AGGCACCTGGCATCCCAGCTACTCCAGGGGCTGAGGTGACAGCATTGCTT
AAGCCCAGAAGGTCGAGGCTGCAGTGAGCTGAGATCACGCCACTGCACTC
CAGTCTGGGTGACAGAGAGAGACCATATCCAAAAAAAAAAAAAAAAAGGG
CGGCCGC

LFDSLSVVLSLSGASPFLGDTKQETLANITAVSYDFDEEFFSQTSELAKDFIRKL
LVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLENFRKQYVRRRWK
LSFSIVSLCNHLTRSLMKKVHLRPDEDLRNCESDTEEDIARRKALHPRRRSSTS

Fig. 4

```
       T   A   L   A   K   E   L   R   E   L   R   I   E   E   T   N   R   P   M      19
  G ACG GCA TTA GCC AAA GAA CTA AGA GAA CTC CGG ATT GAA GAA ACA AAC CGC CCA ATG      57

       K   K   V   T   D   Y   S   S   S   E   E   S   E   S   S   E   E   E      39
  AAG AAG GTG ACT GAT TAC TCC TCC TCC AGT GAG GAG TCA GAA AGT AGC GAG GAA GAG GAG    117

       E   D   G   E   S   E   T   H   D   G   T   V   A   V   S   D   I   P   R   L  59
  GAA GAT GGA GAG AGC GAG ACC CAT GAT GGG ACA GTG GCT GTC AGC GAC ATA CCC AGA CTG   177

       I   P   T   G   A   P   G   S   N   E   Q   Y   N   V   G   M   V   G   T   H  79
  ATA CCA ACA GGA GCT CCA GGC AGC AAC GAG CAG TAC AAT GTG GGA ATG GTG GGG ACG CAT   237

       G   L   E   T   S   H   A   D   S   F   S   G   S   I   S   R   E   G   T   L  99
  GGG CTG GAG ACC TCT CAT GCG GAC AGT TTC AGC GGC AGT ATT TCA AGA GAA GGA ACC TTG   297

       M   I   R   E   T   S   G   E   K   K   R   S   G   H   S   D   S   N   G   F  119
  ATG ATT AGA GAG ACG TCT GGA GAG AAG AAG CGA TCT GGC CAC AGT GAC AGC AAT GGC TTT   357

       A   G   H   I   N   L   P   D   L   V   Q   Q   S   H   S   P   A   G   T   P  139
  GCT GGC CAC ATC AAC CTC CCT GAC CTG GTG CAG CAG AGC CAT TCT CCA GCT GGA ACC CCG   417

       T   E   G   L   G   R   V   S   T   H   S   Q   E   M   D   S   G   T   E   Y  159
  ACT GAG GGA CTG GGG CGC GTC TCA ACC CAT TCC CAG GAG ATG GAC TCT GGG ACT GAA TAT   477

       G   M   G   S   S   T   K   A   S   F   T   P   F   V   D   P   R   V   Y   Q  179
  GGC ATG GGG AGC AGC ACC AAA GCC TCC TTC ACC CCC TTT GTG GAC CCC AGA GTA TAC CAG   537

       T   S   P   T   D   E   D   E   E   D   E   E   S   S   A   A   A   L   F   T  199
  ACG TCT CCC ACT GAT GAA GAT GAA GAG GAT GAG GAA TCA TCA GCC GCA GCT CTG TTT ACT   597

       S   E   L   L   R   Q   E   Q   A   K   L   N   E   A   R   K   I   S   V   V  219
  AGC GAA CTT CTT AGG CAA GAA CAG GCC AAA CTC AAT GAA GCA AGA AAG ATT TCG GTG GTA   657

       N   V   N   P   T   N   I   R   P   H   S   D   T   P   E   I   R   K   Y   K  239
  AAT GTA AAC CCA ACC AAC ATT CGG CCT CAT AGC GAC ACA CCA GAA ATC AGA AAA TAC AAG   717

       K   R   F   N   S   E   I   L   C   A   A   L   W   G   V   N   L   L   V   G  259
  AAA CGA TTC AAC TCA GAA ATA CTT TGT GCA GCT CTG TGG GGT GTA AAC CTT CTG GTG GGG   777

       T   E   N   G   L   M   L   L   D   R   S   G   Q   G   K   V   Y   N   L   I  279
  ACT GAA AAT GGC CTG ATG CTT TTG GAC CGA AGT GGG CAA GGC AAA GTC TAT AAT CTG ATC   837

       N   R   R   R   F   Q   Q   M   D   V   L   E   G   L   N   V   L   V   T   I  299
  AAC CGG AGG GGA TTT CAG CAG ATG GAT GTG CTA GAG GGA CTG AAT GTC CTT GTG ACA ATT   897

       S   G   K   K   N   K   L   R   V   Y   Y   L   S   W   L   R   N   R   I   L  319
  TCA GGA AAG AAG AAT AAG CTA CGA GTT TAC TAT CTT TCA TGG TTA AGA AAC AGA ATA CTA   957

       H   N   D   P   E   V   E   K   K   Q   G   W   I   T   V   G   D   L   E   G  339
  CAT AAT GAC CCA GAA GTA GAA AAG AAA CAA GGC TGG ATC ACT GTT GGG GAC TTG GAA GGC  1017
```

Fig. 5

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C   I   H   Y   K   V   V   K   Y   E   R   I   K   F   L   V   I   A   L   K    359
TGT ATA CAT TAT AAA GTT GTT AAA TAT GAA AGG ATC AAA TTT TTG GTG ATT GCC TTA AAG  1077

N   A   V   E   I   Y   A   W   A   P   K   P   Y   H   K   F   M   A   F   K    379
AAT GCT GTG GAA ATA TAT GCT TGG GCT CCT AAA CCG TAT CAT AAA TTC ATG GCA TTT AAG  1137

S   F   A   D   L   Q   H   K   P   L   L   V   D   L   T   V   E   E   G   Q    399
TCT TTT GCA GAT CTC CAG CAC AAG CCT CTG CTA GTT GAT CTC ACG GTA GAA GAA GGT CAA  1197

R   L   K   V   I   F   G   S   H   T   G   F   H   V   I   D   V   D   S   G    419
AGA TTA AAG GTT ATT TTT GGT TCA CAC ACT GGT TTC CAT GTA ATT GAT GTT GAT TCA GGA  1257

N   S   Y   D   I   Y   I   P   S   H   I   Q   G   N   I   T   P   H   A   I    439
AAC TCT TAT GAT ATC TAC ATA CCA TCT CAT ATT CAG GGC AAT ATC ACT CCT CAT GCT ATT  1317

V   I   L   P   K                                                                444
GTC ATC TTG CCT AAA                                                             1332
```

Fig. 5 (continued)